IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE

CORTEVA AGRISCIENCE LLC,

Plaintiff,

v.

MONSANTO COMPANY and
BAYER CROPSCIENCE LP,

Defendants.

Civil Action No. 22-1046-GBW

Chad S.C. Stover, BARNES & THORNBURG, LLP, Wilmington, Delaware; Michael J. Flibbert, Pier D. DeRoo, Kassandra M. Officer, Rachael P. Dippold, Meredith H. Boerschlein, FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, LLP, New York, New York

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Counsel for Defendants

MEMORANDUM OPINION

September 18, 2023

GREGORY B. WILLIAMS
UNITED STATES DISTRICT JUDGE

Corteva Agriscience LLC ("Plaintiff" or "Corteva") filed suit against Monsanto Company ("Monsanto") and Bayer CropScience LP ("Bayer") (collectively, the Defendants"). Corteva filed its Complaint, D.I. 1, on August 9, 2022, asserting patent infringement of U.S. Patent No. 10,947,555 ("the '555 patent"). On April 17, 2023, Corteva filed for leave to amend its Complaint, which this Court approved on April 21, 2023. That same day, Corteva subsequently filed the First Amended Complaint ("FAC"), D.I. 64, which asserted patent infringement claims for U.S. Patent Nos. 11,149,283 ("the '283 patent") and 11,299,745 ("the '745 patent"), in addition to the '555 patent.[1] On July 14, 2023, Corteva filed its Second Amended Complaint ("SAC"), D.I. 97, adding Count IV (Provisional Rights under 35 U.S.C. § 154(d)) and Count V (Willful Infringement of the Asserted Patents). The parties filed the Joint Claim Construction Chart ("JCCC"), D.I. 82, on June 9, 2023. The parties filed their Joint Claim Construction Brief ("JCCB"), D.I. 137, on August 2, 2023.

Before the Court is the parties' joint request that the Court construe five (5) terms found in the claims of the Asserted Patents. *See* D.I. 137. The Court has reviewed the parties' briefing, D.I. 137, and Joint Claim Construction Chart, D.I. 82, and held a hearing on August 17, 2023. The Court construes the five (5) terms at issue as set forth below.

I. BACKGROUND

The Asserted Patents are entitled "Herbicide Resistance Genes." D.I. 139, Ex. 1 (the '555 patent); D.I. 139, Ex. 2 (the '283 patent); D.I. 139, Ex. 3 (the '067 patent). The Asserted Patents contain overlapping, but not identical, specifications. D.I. 137 at 3 n.1.

[1] The '555 patent, the '283 patent, and the '745 patent are collectively the Asserted Patents.

The Asserted Patents describe transgenic plants comprising of enzymes that are capable of degrading phenoxy auxin and aryloxyphenoxypropionate herbicides. '555 patent at 3:65-5:12. Transgenic plants contain one or more genes that are not naturally present in the plant (i.e., "transgenes"). D.I. 137 at 5. The claims of the patents describe methods for creating a "recombinant polynucleotide" comprising the transgene, which is then introduced into plant cells through genetic transformation techniques to produce transgenic plant cells. *See, e.g.,* '555 patent at claim 1; '283 patent at claim 1; '745 patent at claim 1. The transgenic plants produce a transgene-encoded protein that promotes herbicide tolerance. '555 patent, Abstract. The enzymes and genes used in the Asserted Patents are called AryloxyAlkanoate Dioxygenase ("AAD-1") genes and proteins. *Id.* at 19:52-54, 4:32-46. AAD-1 proteins provide tolerance to combinations of herbicides that can control nearly all broadleaf and grass weeds. *Id.* at 20:13-15. In addition, AAD-1 genes can be "stacked" with other herbicide resistance genes to confer tolerance to additional herbicides. *Id.* at 17:53-57, 20:15-20.

Pending now is the parties' request that the Court construe five (5) disputed terms. D.I. 137. According to their Joint Claim Construction Brief, the parties proposed the following constructions:

	Term	**Corteva's Construction**	**Bayer's Construction**
1	"X_{112} represents a single amino acid at position 112, relative to the sequence of SEQ ID NO: 9" ('555 patent claims 1 and 34; '283 patent, claims 1 and 29; '745 patent, claims 1 and 29)	X_{112} represents a single amino acid that aligns with the amino acid at position 112 of SEQ ID NO: 9 when the amino acid sequence of the AAD-1 protein is aligned with SEQ ID NO:9	X_{112} represents a single amino acid at position 112 in the encoded AAD-1 amino acid sequence, as in the sequence of SEQ ID NO: 9. The single amino acid at position 112 can be any amino acid

	Term	Corteva's Construction	Bayer's Construction
2	"$(X)_{114\text{-}137}$ represents a sequence of 24 amino acids" ('555 patent claims 1 and 34; '283 patent claims 1 and 29; '745 patent claims 1 and 29)	$(X)_{114\text{-}137}$ represents a sequence of 24 amino acids that aligns with the sequence of positions 114-137 of SEQ ID NO: 9 when the amino acid sequence of the AAD-1 protein is aligned with SEQ ID NO:9	$(X)_{114\text{-}137}$ represents a sequence of 24 consecutive amino acids at positions 114-137 in the encoded AAD-1 amino acid sequence, as in the sequence of SEQ ID NO: 9. Each of the 24 consecutive amino acids can be any amino acid
3	"$(X)_{139\text{-}269}$ represents a sequence of 131 amino acids" ('555 patent claims 1 and 34; '283 patent claims 1, 29; '745 patent claims 1 and 29)	$(X)_{139\text{-}269}$ represents a sequence of 131 amino acids that aligns with the sequence of positions 139-269 of SEQ ID NO: 9 when the amino acid sequence of the AAD-1 protein is aligned with SEQ ID NO:9	$(X)_{139\text{-}269}$ represents a sequence of 131 consecutive amino acids at positions 139-269 in the encoded AAD-1 amino acid sequence, as in the sequence of SEQ ID NO: 9. Each of the 131 consecutive amino acids can be any amino acid
4	"$(X)_{271\text{-}280}$ represents a sequence of 10 amino acids" ('555 patent claims 1 and 34; '283 patent claims 1, 29; '745 patent claims 1 and 29)	$(X)_{271\text{-}280}$ represents a sequence of 10 amino acids that aligns with the sequence of positions 271-280 of SEQ ID NO: 9 when the amino acid sequence of the AAD-1 protein is aligned with SEQ ID NO:9	$(X)_{271\text{-}280}$ represents a sequence of 10 consecutive amino acids at positions 271-280 in the encoded AAD-1 amino acid sequence, as in the sequence of SEQ ID NO: 9. Each of the 131 consecutive amino acids can be any amino acid
5	"$(X)_{282\text{-}284}$ represents a sequence of 3 amino acids" ('555 patent claim 2; '283 patent claim 2; '745 patent claim 2)	$(X)_{282\text{-}284}$ represents a sequence of 3 amino acids that aligns with the sequence of positions 282-284 of SEQ ID NO: 9 when the amino acid sequence of the AAD-1 protein is aligned with SEQ ID NO:9	$(X)_{282\text{-}284}$ represents a sequence of 3 consecutive amino acids at positions 282-284 in the encoded AAD-1 amino acid sequence, as in the sequence of SEQ ID NO: 9. Each of the 3 consecutive amino acids can be any amino acid

D.I. 137 at 16, 61-62.

II. LEGAL STANDARDS

"'[T]he claims of a patent define the invention to which the patentee is entitled the right to exclude.'" *Phillips v. AWH Corp.*, 415 F.3d 1303, 1312 (Fed. Cir. 2005) (en banc) (citation omitted); *Aventis Pharms. Inc. v. Amino Chemicals Ltd.*, 715 F.3d 1363, 1373 (Fed. Cir. 2013) (same). "[T]here is no magic formula or catechism for conducting claim construction." *Phillips*, 415 F.3d at 1324. The Court is free to attach the appropriate weight to appropriate sources "in light of the statutes and policies that inform patent law." *Id.* The ultimate question of the proper construction of a patent is a question of law, although "subsidiary factfinding is sometimes necessary." *Teva Pharm. USA, Inc. v. Sandoz, Inc.*, 574 U.S. 318, 326–27 (2015); *see Markman v. Westview Instruments, Inc.*, 517 U.S. 370, 372 (1996) ("the construction of a patent . . . is exclusively within the province of the court.").

"The words of a claim are generally given their ordinary and customary meaning as understood by a person of ordinary skill in the art when read in the context of the specification and prosecution history." *Thorner v. Sony Comput. Entm't Am. LLC*, 669 F.3d 1362, 1365 (Fed. Cir. 2012) (citing *Phillips*, 415 F.3d at 1313); *Unwired Planet, LLC v. Apple Inc.*, 829 F.3d 1353, 1358 (Fed. Cir. 2016) (similar). The "'only two exceptions to this general rule'" are (1) when a patentee defines a term or (2) disavowal of "'the full scope of a claim term either in the specification or during prosecution.'" *Thorner*, 669 F.3d at 1365 (citation omitted).

The Court "'first look[s] to, and primarily rel[ies] on, the intrinsic evidence,'" which includes the claims, written description, and prosecution history and "'is usually dispositive.'" *Personalized Media Commc'ns, LLC v. Apple Inc.*, 952 F.3d 1336, 1340 (Fed. Cir. 2020) (citation omitted). "[T]he specification ' . . . is the single best guide to the meaning of a disputed term.'" *Akzo Nobel Coatings, Inc. v. Dow Chem. Co.*, 811 F.3d 1334, 1340 (Fed. Cir. 2016)

(citation omitted). "'[T]he specification may reveal a special definition given to a claim term by the patentee that differs from the meaning it would otherwise possess.' When the patentee acts as its own lexicographer, that definition governs." *Cont'l Cirs. LLC v. Intel Corp.*, 915 F.3d 788, 796 (Fed. Cir. 2019) (quoting *Phillips*, 415 F.3d at 1316). However, "'[the Court] do[es] not read limitations from the embodiments in the specification into the claims.'" *MasterMine Software, Inc. v. Microsoft Corp.*, 874 F.3d 1307, 1310 (Fed. Cir. 2017) (citation omitted)). The "written description . . . is not a substitute for, nor can it be used to rewrite, the chosen claim language." *SuperGuide Corp. v. DirecTV Enters., Inc.*, 358 F.3d 870, 875 (Fed. Cir. 2004).

The Court "should also consider the patent's prosecution history, if it is in evidence." *Markman v. Westview Instruments, Inc.*, 52 F.3d 967, 980 (Fed. Cir. 1995), *aff'd*, 517 U.S. 370; *Cont'l Cirs.*, 915 F.3d at 796 (same). The prosecution history may "'demonstrat[e] how the inventor understood the invention and whether the inventor limited the invention in the course of prosecution . . . ." *SpeedTrack, Inc. v. Amazon.com*, 998 F.3d 1373, 1377 (Fed. Cir. 2021) (quoting *Phillips*, 415 F.3d at 1317).

The Court may "need to look beyond the patent's intrinsic evidence and to consult extrinsic evidence in order to understand, for example, the background science or the meaning of a term in the relevant art during the relevant time period." *Teva*, 574 U.S. at 331. "Extrinsic evidence consists of all evidence external to the patent and prosecution history, including expert and inventor testimony, dictionaries, and learned treatises." *Markman*, 52 F.3d at 980; *Phillips*, 415 F.3d at 1317 (same). Extrinsic evidence may be useful, but it is "less significant than the intrinsic record in determining the legally operative meaning of claim language." *Cont'l Cirs.*, 915 F.3d at 799 (internal quotation marks and citations omitted). However, "[p]atent documents are written for persons familiar with the relevant field . . . . Thus resolution of any ambiguity

arising from the claims and specification may be aided by extrinsic evidence of usage and meaning of a term in the context of the invention." *Verve, LLC v. Crane Cams, Inc.*, 311 F.3d 1116, 1119 (Fed. Cir. 2002); *see Nautilus, Inc. v. Biosig Instruments, Inc.*, 572 U.S. 898, 899 (2014) (explaining that patents are addressed "to those skilled in the relevant art").

III. AGREED-UPON CONSTRUCTIONS

The parties agree that, for the purposes of this action, the following terms are not in dispute and do not require construction. D.I. 137 at 16.

	Term
1	"A transgenic plant cell" ('555 patent)
2	"A transgenic plant" ('555 patent)
3	"an AAD-1 protein that exhibits aryloxyalkanoate dioxygenase activity wherein said activity enzymatically degrades a phenoxy auxin herbicide and an (R)- aryloxyphenoxypropionate herbicide" ('555, '283, and '745 patents)

IV. CONSTRUCTION OF DISPUTED TERMS

The following five (5) terms are in dispute, require construction, and are construed as set for below for the reasons herein.

A. Term 1

Term No.	Term	Corteva's Construction	Bayer's Construction	Court's Construction
1	"X_{112} represents a single amino acid at position	X_{112} represents a single amino acid that aligns with the	X_{112} represents a single amino acid at position 112 in the	X_{112} represents a single amino acid that aligns with the

	112, relative to the sequence of SEQ ID NO: 9" (the '555 patent, claims 1 and 34; the '283 patent, claims 1 and 29; the '745 patent, claims 1 and 29)	amino acid at position 112 of SEQ ID NO: 9 when the amino acid sequence of the AAD-1 protein is aligned with SEQ ID NO: 9.	encoded AAD-1 amino acid sequence, as in the sequence of SEQ ID NO: 9. The single amino acid at position 112 can be any amino acid.	amino acid at position 112 of SEQ ID NO: 9 when the amino acid sequence of the AAD-1 protein is aligned with SEQ ID NO: 9.

The question is whether the subscript numbers for X in Term 1 represent fixed positions or positions relative to its alignment. Bayer proposes that Term 1 be construed such that the "AAD-1 motif" refers to specific positions in the amino acid sequence "as in the sequence of SEQ ID NO: 9," while Corteva proposes that it be construed to require "align[ment] with SEQ ID NO: 9." D.I. 137 at 18, 25.

First, the Court looks to the claim language. The term is shown in the first claim of the '555 patent below:

1. A transgenic plant cell comprising a recombinant polynucleotide that encodes an AAD-1 protein that exhibits aryloxyalkanoate dioxygenase activity wherein said activity enzymatically degrades a phenoxy auxin herbicide and an (R)-aryloxyphenoxypropionate herbicide, further wherein said AAD-1 protein comprises:

    i) an amino acid sequence having at least 85% sequence identity with SEQ ID NO: 9; and
    ii) an AAD-1 motif having the general formula of:

    $HX_{112}D(X)_{114\text{-}137}T(X)139\text{-}269H(X)_{271\text{-}280}R$, wherein

    X_{112} represents a single amino acid at position 112, relative to the sequence of SEQ ID NO: 9; **[Term 1]**

'555 patent at claim 1.

First, Corteva urges the Court to consider Term 1 in the context of claim 1 as a whole, including subparts i) and ii) of claim 1. *See, e.g., IGT v. Bally Gaming Int'l, Inc.*, 659 F.3d 1109, 1117 (Fed. Cir. 2011) ("We caution that claim language must be construed in the context of the claim in which it appears. Extracting a single word from a claim divorced from the surrounding limitations can lead construction astray."). In order to determine the percentage identity necessary to meet subpart i) of claim 1, the specification provides the following: "[p]ercent identity [is] determined by translating both the rdpA and tfdA DNA sequences deposited in the database to proteins, then using ClustalW in the VectorNTI software package to perform the multiple sequence alignment." '555 patent at 44:40-44. Corteva asserts that because multiple sequence alignment is required to determine the prerequisite 85% percent identity, sequence alignment is required to meet at least subpart i) of the claim. D.I. 137 at 19. But claims must be read as a whole, and thus Corteva reasons that subpart ii) of claim 1 also requires sequence alignment. *Id.*

Subpart ii) requires the AAD-1 motif as having the general formula of: $HX_{112}D(X)_{114\text{-}137}T(X)_{139\text{-}269}H(X)_{271\text{-}280}R$, "wherein X_{112} represents a single amino acid at position 112, ***relative to*** the sequence of SEQ ID NO: 9[.]" '555 patent at claim 1 (emphasis added). That "relative to" language, Corteva asserts, references the alignment with the SEQ ID NO:9, which determines location of the amino acids in the sequence. D.I. 137 at 18-19. Bayer, in contrast, argues that the number denoting X refers to a fixed position.[2]

[2] "At the outset, Bayer's proposed constructions specify that "X" can be "any amino acid." Corteva's proposed constructions do not address the meaning of "X," although Corteva admits that Bayer's position is correct, stating "amino acids are denoted with an 'X' (meaning they can be any amino acid)." Br. 7. That aspect of the parties' constructions is therefore not in dispute." D.I. 137 at 24-25.

Bayer asserts that its construction requiring fixed positions is proper because to find otherwise would be to render the subscript numbers unnecessary:

> There would have been no need to change the numbering convention used in the position-neutral generic prior art motif after "mapping" it onto SEQ ID NO: 9. Indeed, that change would have been unnecessary, because the only function served by each of the four subscript numbers in the "AAD-1 motif" ("112", "114-137," "139-269," and "271-280") is to identify the positions of the unspecified amino acids in each spacer. Otherwise, reciting positions 114-137 in "$(X)_{114\text{-}137}$" would have no meaning at all, because "$(X)_{114\text{-}137}$" would cover not only a sequence of any amino acids at positions 114-137, but also a sequence of any amino acids at positions 115-138, or a sequence of any amino acids at positions 116-139, or a sequence of any amino acids at 164-187, and so on.

D.I. 137 at 25-26.

Both parties assert that the other's construction renders claim language superfluous. According to Bayer, in a genal prior art motif, the numeric subscripts refer to the lengths of the spacers, not positions, and thus require alignment to a subject sequence before the position of the motif within that sequence can be determined. *Id.* Bayer looks ahead to the following Terms 2-5 in claim 1, which states that "$(X)_{114\text{-}137}$ represents a sequence of 24 amino acids" (Term 2) to show that 114-137 must be the location because the "sequence of 24 amino acids" acts as the qualifying spacer language. *Id.*

Meanwhile, Corteva argues that Bayer's construction writes out the "relative to the sequence of SEQ ID NO: 9." Corteva asserts that, in the event the subscript is a fixed location, the "relative to" language would be rendered superfluous as the claim could just as easily read: X_{112} represents a single amino acid at position 112[.]~~, relative to the sequence of SEQ ID NO: 9~~. D.I. 137 at 40.

For additional clarification, the Court looks to the specification. *Phillips*, 415 F.3d at 1313 ("Importantly, the person of ordinary skill in the art is deemed to read the claim term not

only in the context of the particular claim in which the disputed term appears, but in the context of the entire patent, including the specification.").

The specification of the '555 patent describes three AAD-1 protein variants, which are referred to as AAD-1 v1, AAD-1 v2, and AAD-1 v3. '555 patent at 6:56-63. Their amino acid sequences are disclosed in SEQ ID NOS: 9, 10, and 11, respectively. *Id.*

The AAD-1 motif in SEQ ID NO: 11 is shifted by one amino acid in location such that the residue at position 112 in SEQ ID NO: 9 is at position 113 in SEQ ID NO: 11. *Id.* at 20. Corteva argues that this minor shift in the motif's position is irrelevant to the invention because SEQ ID NO: 11, when aligned with SEQ ID NO: 9, contains the same pattern of conserved amino acids (the AAD-1 motif) as protein variants AAD-1 v1, AAD-1 v2. *Id.* at 20. *See also* '555 patent at 6:44-50 (explaining that SEQ ID NO:11 is the same as SEQ ID NO:9 but for the addition of an alanine residue at the second position). But because Bayer is arguing that the subscript to X is a fixed location, Bayer's construction would write out AAD-1 v3.

The specification of the '555 patent describes these three AAD-1 protein variants and their amino acid sequences. '555 patent at 6:56-63. Throughout the specification, all three of these protein variants are described as part of the invention and appear to reflect the preferred embodiments. D.I. 137 at 2. The specification explains that the AAD-1 v3 variant of SEQ ID NO: 11 results from optimizing the AAD-1 gene for expression in plants. *Id.* at 58:26-37. The plant-optimized AAD-1 v3 variant is discussed extensively throughout the specification, appearing over 230 times in the text. *Id.*, Examples 5-9, 11-14, and 17-26; Tables 14-29, 32, and 35-38; Figs. 8A, 8B, 9A-9C, 10-18, 20, and 21. In fact, the AAD-1 v3 variant is the subject of its own experiments. *Id.*, Tables 17-29, 32, 35-38. Moreover, the specification reports that

AAD-1v3 provided "a significant advantage" for 2,4-D resistance in planta compared to AAD-1v2. *See id.* at 117:50-64; *see also* 69:15-19.

To write out a preferred embodiment requires high evidentiary support. *SynQor, Inc. v. Artesyn Techs., Inc.*, 709 F.3d 1365, 1378-79 (Fed. Cir. 2013) ("A claim construction that 'excludes the preferred embodiment is rarely, if ever, correct and would require highly persuasive evidentiary support.'") (quoting *Adams Respiratory Therapeutics, Inc. v. Perrigo Co.*, 616 F.3d 1283, 1290 (Fed. Cir. 2010)). Bayer provides its support below.

First, Bayer argues that Corteva could have and failed to incorporate "align" into the claim language. D.I. 137 at 25-27. Bayer cites to earlier patents owned by Corteva to show that, in the event Corteva wanted the claim language to require alignment, it knew how to write it as such. *Id.*

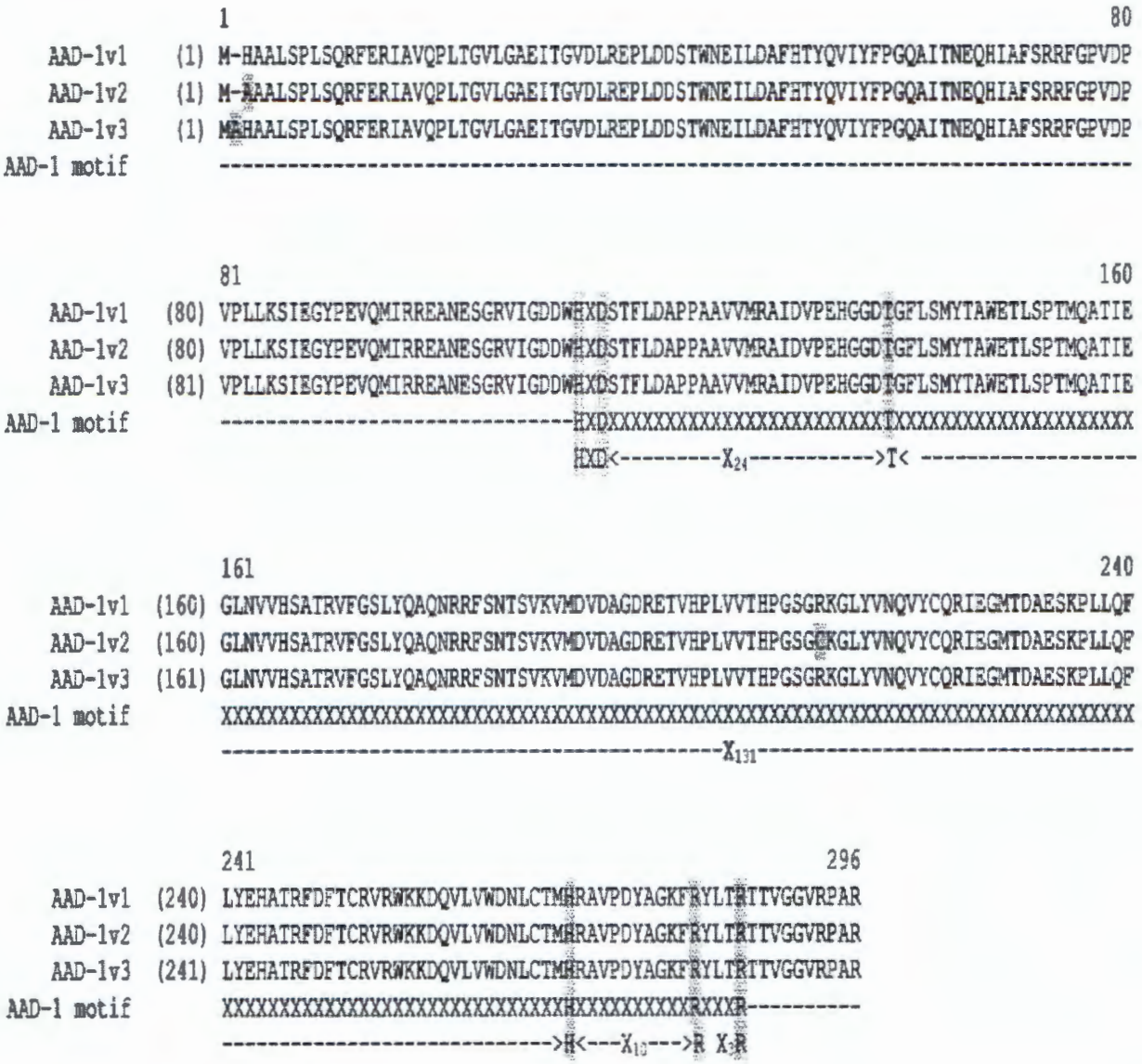
Corteva owns an earlier U.S. Patent No. 9,382,549 (the "'549 patent"), which shares a named inventor with the Asserted Patents. D.I. 139, Ex. 11. Like the Asserted Patents, the '549 patent relates to transgenic plants and plant cells that comprise specific amino acid sequences. But unlike the Asserted Patents, the '549 patent expressly requires the claimed amino acid sequences to be "aligned" with the '549 patent's listed amino acid sequences. Claim 1 states: "1. A polynucleotide . . . wherein the polynucleotide encodes a polypeptide having at least 95% sequence identity with the amino acid sequence of SEQ ID NO:1, ***that when aligned with SEQ ID NO:1***, comprises an alanine at the position corresponding to position 84 of SEQ ID NO:1 and/or a threonine at the position corresponding to position 172 of SEQ ID NO:1." D.I. 139, Ex.

11 (the '549 patent), claim 1 (emphasis added).[3] Thus, Bayer asserts that Corteva knew how to claim "alignment" when it wanted to, but deliberately chose not to do so here.

However, the '549 patent claims a different invention, has a different specification and prosecution history, and was filed years before the '555 patent. Courts do not require that constructions be consistent across such patents. *See Trustees of Columbia Univ. in City of New York v. Symantec Corp.*, 811 F.3d 1359, 1369 (Fed. Cir. 2016) (finding that constructions of claim terms across patents need not be the same where the patents at issue were from two separate families, claimed two different inventions, listed only one inventor in common, were filed years apart, and did not result from the same patent application).

Bayer next asserts that there is a position-neutral generic prior art motif necessitates "alignment." D.I. 137 at 27-28. During the prosecution, inventor Dr. Wright and Dr. Nair submitted declarations that performed the alignment of AAD-1 v3. D.I. 139, Ex. 8 at JA00998; JA1089. Below is the sequence alignment performed by Dr. Satish Nair, during the prosecution of the '555 patent:

[3] Corteva argues that this shows how sequence alignments are routinely used in the art to compare amino acid sequences. D.I. 137 at 29.



D.I. 139, Ex. 8 at JA1089.

The alignment is a "[d]emonstration how the three enabled AAD-1 variant enzymes . . . conforms to the specific AAD-1 motif $HXDX_{24}TX_{131}HX_{10}R$." *Id.* Notably, the sequence of AAD-1 v3 is shifted to account for its extra amino acid in the second position. But the motif used in the declaration is position-neutral—the motif, Bayer asserts, Corteva would have used for its claims if alignment were required. D.I. 137 at 25-26.

The Court is unconvinced that failure to use the position-neutral motif in the claim language results in a surrendering of a construction that requires alignment, especially when the claim is read as a whole.

At the outset, the claim language "relative to SEQ ID NO:9" reads to the Court that the motif should be aligned with SEQ ID NO:9. Corteva is correct that the claim should be read as a whole, and Claim 1 has two subparts, both of which need to be met. Subpart i) requires the AAD-1 protein comprises of an amino acid with an 85% sequence identity with SEQ ID NO: 9, which according to the specification requires an alignment. '555 patent at 44:40-44. Subpart ii) provides the AAD-1 motif having a formula of:

> $HX_{112}D(X)_{114\text{-}137}T(X)_{139\text{-}269}H(X)_{271\text{-}280}R$, wherein
>
> X_{112} represents a single amino acid at position 112, relative to the sequence of SEQ ID NO: 9[.]

Corteva's construction makes use of the claim language "relative to the sequence of SEQ ID NO:9" by providing this Court with a construction that explains how the position is dependent on the alignment with SEQ ID NO:9. *Wasica Fin. GmbH v. Cont'l Auto. Sys., Inc.*, 853 F.3d 1272, 1288 n.10 (Fed. Cir. 2017) ("It is highly disfavored to construe terms in a way that renders them void, meaningless, or superfluous."). Corteva's construction also encompasses the three preferred AAD-1 motif embodiments in the specification. "[A] claim interpretation that excludes a preferred embodiment from the scope of the claim is rarely, if ever, correct." *MBO Lab'ys, Inc. v. Becton, Dickinson & Co.*, 474 F.3d 1323, 1333 (Fed. Cir. 2007) (rejecting the district court's construction that wrote out two different preferred embodiments depicted in figures of the asserted patent). *See also bioMerieux, S.A. v. Hologic, Inc.*, No. CV 18-21-LPS, 2019 WL 2436351, at *4 (D. Del. June 11, 2019) ("Thus, adoption of Defendants' proposed construction would lead to exclusion of a preferred embodiment, which is not a preferred

result."); *Power Integrations, Inc. v. Fairchild Semiconductor Int'l, Inc.*, 904 F.3d 965, 972 (Fed. Cir. 2018) ("where the claim language permits an operable construction, the inoperable construction is wrong." (citing *Ecolab, Inc. v. FMC Corp.*, 569 F.3d 1335, 1345 (Fed. Cir. 2009))). Indeed, the intrinsic evidence is one-sided, in favor of Corteva's construction.

Bayer cites to *Cordis Corp. v. Medtronic AVE, Inc.*, 511 F.3d 1157 (Fed. Cir. 2008) and *Acumed LLC v. Stryker Corp.*, 483 F.3d 800 (Fed. Cir. 2007) for the assertion that Corteva knew it could use the term aligned, as it did in other patents, and chose not to here. Therefore, Bayer contends the Court should not accept Corteva's proposal that reads in "aligned." However, these cases cited by Bater are distinguishable because the language that patentee could have used in the claim language was used in the intrinsic evidence but not used in the claims. In *Cordis*,

> The initial reference to "alternating slots" refers to the half-slots at the end of the tubular member. Although the written description adopts a more specific term for those slots ('half-slots'), that does not foreclose the generic term "slots" from being used to refer to both half slots and complete slots. The written description uses the more specific phrase 'complete slots' when distinguishing complete slots from half slots, and thus supports the inference that the term 'slots,' as used in claim 23, refers to both complete slots and half slots. If the patentee had intended claim 23 to only cover grafts with tubular members having complete slots, the patentee presumably would have drafted the claim to specify 'complete slots,' the term used in the written description to describe such fully bounded slots.

511 F.3d at 1174 (emphasis added); *see also Acumed LLC* 483 F.3d at 807 ("The intrinsic evidence of the specification therefore suggests that the patentees knew how to restrict their claim coverage to holes passing through at right angles. They could have used the word 'perpendicular,' as they did in discussing their preferred embodiment.")

Those cases are distinguishable. The Federal Circuit relied on evidence in the specification that showed the patentee knew how to narrow the claims in each case and chose not to. *Cordis Corp.*, 511 F.3d at 1174; *Acumed LLC* 483 F.3d at 807. Here, Bayer failed to cite conflicting language in the intrinsic record to support its argument.

In comparing Corteva's construction to Bayer's, it is clear that Bayer seeks to cut out (1) a healthy portion of the claim language, and (2) a preferred embodiment. First, Bayer's construction would render the claim to read as follows:

1. A transgenic plant cell comprising a recombinant polynucleotide that encodes an AAD-1 protein that exhibits aryloxyalkanoate dioxygenase activity wherein said activity enzymatically degrades a phenoxy auxin herbicide and an (R)-aryloxyphenoxypropionate herbicide, further wherein said AAD-1 protein comprises:

    iii) an amino acid sequence having at least 85% sequence identity with SEQ ID NO: 9; and
    iv) an AAD-1 motif having the general formula of:

    $HX_{112}D(X)_{114\text{-}137}T(X)139\text{-}269H(X)_{271\text{-}280}R$, wherein

    X_{112} represents a single amino acid at position 112, ~~relative to the sequence of SEQ ID NO: 9;~~

    $(X)_{114\text{-}137}$ ~~represents a sequence of 24 amino acids;~~ [Term 2]

    $(X)_{139\text{-}269}$ ~~represents a sequence of 131 amino acids; and~~ [Term 3]

    $(X)_{271\text{-}280}$ ~~represents a sequence of 10 amino acids.~~ [Term 4]

Moreover, Bayer's assertion that Corteva's construction writes out the "representations of a sequence of X amino acids," is unconvincing. Each spacer (X) in the AAD-1 motif is defined by its (1) position relative to the sequence of SEQ ID NO: 9, and (2) number of amino acids within each spacer; thus, this Court finds that there is nothing superfluous (or "self-erasing") about those structural definitions.

Second, Bayer's construction would also write out a preferred embodiment and failed to provide the high evidentiary support to do so. *SynQor, Inc.*, 709 F.3d at 1378-79. Instead, when reviewing the prosecution history of the '555 patent, the Court notes that Corteva and the examiner always considered the preferred AAD-1 v3 variant as part of the claimed invention.

See, e.g., D.I. 139, Ex. 8 at JA0998; JA1089 (Declarations wherein AAD-1 v3 variant was aligned to conform to the AAD-1 motif).

For these reasons, the Court will accept Corteva's construction of Term 1.

B. Terms 2-5

Terms 2-5 are exemplified in Claims 1 and 2 of the '555 patent below:

1. A transgenic plant cell comprising a recombinant polynucleotide that encodes an AAD-1 protein that exhibits aryloxyalkanoate dioxygenase activity wherein said activity enzymatically degrades a phenoxy auxin herbicide and an (R)-aryloxyphenoxypropionate herbicide, further wherein said AAD-1 protein comprises:

   i) an amino acid sequence having at least 85% sequence identity with SEQ ID NO: 9; and
   ii) an AAD-1 motif having the general formula of:

   $HX_{112}D(X)_{114\text{-}137}T(X)139\text{-}269H(X)_{271\text{-}280}R$, wherein

   X_{112} represents a single amino acid at position 112, relative to the sequence of SEQ ID NO: 9;

   $(X)_{114\text{-}137}$ represents a sequence of 24 amino acids; **[Term 2]**

   $(X)_{139\text{-}269}$ represents a sequence of 131 amino acids; and **[Term 3]**

   $(X)_{271\text{-}280}$ represents a sequence of 10 amino acids. **[Term 4]**

2. The plant cell of claim 1 wherein said AAD-1 motif has the general formula of:

   $HX_{112}D(X)_{114\text{-}137}T(X)_{139\text{-}269}H(X)_{271\text{-}280}R(X)_{282\text{-}284}R$,

   wherein $(X)_{282\text{-}284}$ represents a sequence of 3 amino acids. **[Term 5]**

D.I. 139, Ex. 1 (the '555 patent) claim 1.

The parties agree that the construction of Terms 2-5 should be consistent with the Court's construction of Term 1. D.I. 137 at 62-65. For all the reasons given above for Term 1, the Court will adopt Corteva's constructions for Terms 2-5.

V. CONCLUSION

The Court will construe the disputed claim terms as described above. The Court will issue an Order consistent with this Memorandum Opinion.